SEQUENCE LISTING

- (1) GENERAL INFORMATION:
 - (i) APPLICANT: Trustees of the University of Pennsylvania Wilson, James M. Fisher, Krishna J.
 - (ii) TITLE OF INVENTION: Method for Recombinant Adeno-Associated Virus-Directed Gene Therapy
 - (iii) NUMBER OF SEQUENCES: 4
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Howson and Howson
 - (B) STREET: Spring House Corporate Cntr, PO Box 457
 - (C) CITY: Spring House
 - (D) STATE: Pennsylvania
 - (E) COUNTRY: USA (F) ZIP: 19477
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk

 - (B) COMPUTER: IBM PC compatible (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
 - (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: WO (B) FILING DATE:

 - (C) CLASSIFICATION:
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/708,188
 - (B) FILING DATE: 06-SEP-1996
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/729,061
 (B) FILING DATE: 10-OCT-1996
 - (viii) ATTORNEY/AGENT INFORMATION:

 - (A) NAME: Kodroff, Cathy A. (B) REGISTRATION NUMBER: 33,980
 - (C) REFERENCE/DOCKET NUMBER: GNVPN.019CIP2PCT
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 215-540-9200
 - (B) TELEFAX: 215-540-5818
- (2) INFORMATION FOR SEQ ID NO:1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10398 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

(XI) SEQUENCE DESCRIPTION: SEQ ID NO.1.		
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TGACGTTTTT GGTGTGCGCC GGTGTACACA GGAAGTGACA ATT	TTTCGCGC GGTTTTAGGC 2	240
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GGGCGACCTT TGGTCGCCCG GCCTCAGTGA GCGAGCGAGC GCG	CAGAGAG GGAGTGGCCA	180
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ATCCCGTCGT TTTACAACGT CGTGACTGGG AAAACCCTGG CG	TTACCCAA CTTAATCGCC 1	560
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AAGCGGTGCC GGAAAGCTGG CTGGAGTGCG ATCTTCCTGA GG	CCGATACT GTCGTCGTCC 1	740
CCTCAAACTG GCAGATGCAC GGTTACGATG CGCCCATCTA CA	CCAACGTA ACCTATCCCA 1	800
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ACTCGGCGTT	* TCATCTGTGG	TGCAACGGGC	GCTGGGTCGG	TTACGGCCAG	GACAGTCGTT	1980
TGCCGTCTGA	ATTTGACCTG	AGCGCATTTT	TACGCGCCGG	AGAAAACCGC	CTCGCGGTGA	2040
TGGTGCTGCG	TTGGAGTGAC	GGCAGTTATC	TGGAAGATCA	GGATATGTGG	CGGATGAGCG	2100
GCATTTTCCG	TGACGTCTCG	TTGCTGCATA	AACCGACTAC	ACAAATCAGC	GATTTCCATG	2160
TTGCCACTCG	CTTTAATGAT	GATTTCAGCC	GCGCTGTACT	GGAGGCTGAA	GTTCAGATGT	2220
GCGGCGAGTT	GCGTGACTAC	CTACGGGTAA	CAGTTTCTTT	ATGGCAGGGT	GAAACGCAGG	2280
TCGCCAGCGG	CACCGCGCCT	TTCGGCGGTG	AAATTATCGA	TGAGCGTGGT	GGTTATGCCG	2340
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TCCAGTTCCG	TTTATCCGGG	CAAACCATCG	AAGTGACCAG	CGAATACCTG	TTCCGTCATA	3420
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AAGTGCCTCT	GGATGTCGCT	CCACAAGGTA	AACAGTTGAT	TGAACTGCCT	GAACTACCGC	3540
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	CACCGCTGGA	TAACGACATT	GGCGTAAGTG	AAGCGACCCG	CATTGACCCT	AACGCCTGGG	3900
	TCGAACGCTG	GAAGGCGGCG	GGCCATTACC	AGGCCGAAGC	AGCGTTGTTG	CAGTGCACGG	3960
	CAGATACACT	TGCTGATGCG	GTGCTGATTA	CGACCGCTCA	CGCGTGGCAG	CATCAGGGGA	4020
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	GGCGGTAAAC	ATATTAGGAA	CCAGCCTGTG	ATGCTGGATG	TGACCGAGGA	GCTGAGGCCC	5340
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	CAGGTTTCTG	CCCTGAAGGC	TTCCTCCCCT	CCCAATGCGG	TTTAAAACAT	АААТААААА	5940
	CCAGACTCTG	TTTGGATTTG	GATCAAGCAA	GTGTCTTGCT	GTCTTTATTT	AGGGGTTTTG	6000
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	GGCAGGCCCT	TGGTGTAAGT	GTTTACAAAG	CGGTTAAGCT	GGGATGGGTG	CATACGTGGG	6300
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•	TTTCGCTGTA	CGGCAGTAGT	CGGTGCTCGT	CCAGACGGGC	CAGGGTCATG	TCTTTCCACG	7200
4	GGCGCAGGGT	CCTCGTCAGC	GTAGTCTGGG	TCACGGTGAA	GGGGTGCGCT	CCGGGCTGCG	7260
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GGCTGTGTGC	ACGAACCCCC	CGTTCAGCCC	GACCGCTGCG	CCTTATCCGG	TAACTATCGT	8880
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TCTACGGGGT	CTGACGCTCA	GTGGAACGAA	AACTCACGTT	AAGGGATTTT	GGTCATGAGA	9240
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CGCTCACCGG	CTCCAGATTT	ATCAGCAATA	AACCAGCCAG	CCGGAAGGGC	CGAGCGCAGA	9540

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GTGTCACGCT	CGTCGTTTGG	TATGGCTTCA	TTCAGCTCCG	GTTCCCAACG	ATCAAGGCGA	9720
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(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid

 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: other nucleic acid
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CATGGTAATA GCGATGACTA

20

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs

 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: other nucleic acid
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCTCTGCTTA TATAGACCTC

- (2) INFORMATION FOR SEQ ID NO:4:
 - (i) SEQUENCE CHARACTERISTICS:

 (A) LENGTH: 20 base pairs

 (B) TYPE: nucleic acid

 (C) STRANDEDNESS: single

 (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: other nucleic acid
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATAAGCTGCA ATAAACAAGT